

JUN 10 2003

TECH CENTER



1600

RAW SEQUENCE LISTING

DATE: 05/27/2003

PATENT APPLICATION: US/08/812,393B

TIME: 15:09:37

Input Set : A:\46155793.app

Output Set: N:\CRF4\05272003\H812393B.raw

3 <110> APPLICANT: SHERMAN, LINDA A.
4 LUSTGARTEN, JOSEPH
6 <120> TITLE OF INVENTION: RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS
7 SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS
9 <130> FILE REFERENCE: 46147/55793
11 <140> CURRENT APPLICATION NUMBER: 08/812,393B
12 <141> CURRENT FILING DATE: 1997-03-05
14 <160> NUMBER OF SEQ ID NOS: 64
16 <170> SOFTWARE: PatentIn Ver. 2.1
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1350
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1332)
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
29 single chain TCR derivative nucleotide sequence
31 <400> SEQUENCE: 1
32 ctc gag atg cag agg aac ctg gga gct gtg ctg ggg att ctg tgg gtg 48
33 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
34 1 5 10 15
36 cag att tgc tgg ctg aaa gaa cag caa gtg cag cag agt ccc gca tcc 96
37 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
38 20 25 30
40 ttg gtt ctg cag gag ggg gag aac gca gag ctc cag tgt agc ttt tcc 144
41 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
42 35 40 45
44 atc ttt aca aac cag gtg cag tgg ttt tac caa cgt cct ggg gga aga 192
45 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
46 50 55 60
48 ctc gtc agc ctg ttg tac aat cct tct ggg aca aag cag agt ggg aga 240
49 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
50 65 70 75 80
52 ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att 288
53 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
54 85 90 95
56 tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat 336
57 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
58 100 105 110
60 tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc 384
61 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu

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62	115	120	125	
64	tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432		
65	Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly			
66	130	135	140	
68	gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480		
69	Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala			
70	145	150	155	160
72	gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528		
73	Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His			
74	165	170	175	
76	aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576		
77	Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu			
78	180	185	190	
80	atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624		
81	Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro			
82	195	200	205	
84	gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672		
85	Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile			
86	210	215	220	
88	ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720		
89	Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser			
90	225	230	235	240
92	ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768		
93	Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys			
94	245	250	255	
96	ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816		
97	Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val			
98	260	265	270	
100	ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864		
101	Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro			
102	275	280	285	
104	cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912		
105	Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro			
106	290	295	300	
108	tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc	960		
109	Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu			
110	305	310	315	320
112	ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc	1008		
113	Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe			
114	325	330	335	
116	agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc	1056		
117	Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu			
118	340	345	350	
120	tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac	1104		
121	Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp			
122	355	360	365	
124	aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag	1152		
125	Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys			
126	370	375	380	

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128 aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg      1200
129 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
130 385                               390                               395                               400
132 gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag      1248
133 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
134                               405                               410                               415
136 ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc      1296
137 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
138                               420                               425                               430
140 tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc      1344
141 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
142                               435                               440
144 acc gcg                                                                1350
147 <210> SEQ ID NO: 2
148 <211> LENGTH: 444
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
154     single chain TCR protein
156 <400> SEQUENCE: 2
157 Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
158 1      5      10      15
160 Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
161      20      25      30
163 Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
164      35      40      45
166 Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg
167      50      55      60
169 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg
170      65      70      75      80
172 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile
173      85      90      95
175 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn
176      100     105     110
178 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu
179      115     120     125
181 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
182      130     135     140
184 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala
185      145     150     155     160
187 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His
188      165     170     175
190 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu
191      180     185     190
193 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro
194      195     200     205
196 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile
197      210     215     220

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199 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser
200 225                230                235                240
202 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys
203                245                250                255
205 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val
206                260                265                270
208 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro
209                275                280                285
211 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
212                290                295                300
214 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
215 305                310                315                320
217 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
218                325                330                335
220 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
221                340                345                350
223 Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
224                355                360                365
226 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
227                370                375                380
229 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
230 385                390                395                400
232 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
233                405                410                415
235 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
236                420                425                430
238 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
239                435                440
242 <210> SEQ ID NO: 3
243 <211> LENGTH: 24
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
250 <400> SEQUENCE: 3
251 cccaaggcac tgatgttcat cttc                                     24
254 <210> SEQ ID NO: 4
255 <211> LENGTH: 27
256 <212> TYPE: DNA
257 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
260 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
262 <400> SEQUENCE: 4
263 tgagacaaag tccccaatct ctgacag                                     27
266 <210> SEQ ID NO: 5
267 <211> LENGTH: 26
268 <212> TYPE: DNA
269 <213> ORGANISM: Artificial Sequence
271 <220> FEATURE:

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272 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
274 <400> SEQUENCE: 5
275 ctgcagctgc tcctcaagta ctattc 26
278 <210> SEQ ID NO: 6
279 <211> LENGTH: 28
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
283 <220> FEATURE:
284 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
286 <400> SEQUENCE: 6
287 tcccggagaa ggtccacagt tcctcttt 28
290 <210> SEQ ID NO: 7
291 <211> LENGTH: 29
292 <212> TYPE: DNA
293 <213> ORGANISM: Artificial Sequence
295 <220> FEATURE:
296 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
298 <400> SEQUENCE: 7
299 gaagcagcag agggtttgaa gccacatac 29
302 <210> SEQ ID NO: 8
303 <211> LENGTH: 27
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
310 <400> SEQUENCE: 8
311 ggcaggtctt cagttgctta tgaaggt 27
314 <210> SEQ ID NO: 9
315 <211> LENGTH: 27
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
322 <400> SEQUENCE: 9
323 ggttcctctt caggggtccag aatatgt 27
326 <210> SEQ ID NO: 10
327 <211> LENGTH: 27
328 <212> TYPE: DNA
329 <213> ORGANISM: Artificial Sequence
331 <220> FEATURE:
332 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
334 <400> SEQUENCE: 10
335 gcgaagaact caccctggac tgttcat 27
338 <210> SEQ ID NO: 11
339 <211> LENGTH: 30
340 <212> TYPE: DNA
341 <213> ORGANISM: Artificial Sequence
343 <220> FEATURE:
344 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/08/812,393B

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Input Set : A:\46155793.app
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Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 239

VERIFICATION SUMMARY

DATE: 05/27/2003

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Input Set : A:\46155793.app

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